AMENDMENTS TO THE SPECIFICATION:

Kindly replace the paragraph beginning on page 15, line 25, with the following amended paragraph:

FIGS. 11A and **11B.** DNA and amino acid sequences (SEQ ID NOS.: 51-52) of the mouse 21.6 light chain variable region respectively.

Kindly replace the paragraph beginning on page 15, line 27, with the following amended paragraph:

FIGS. 12A and **12B.** DNA and amino acid sequences (SEQ ID NOS.: 53-54) of the mouse 21.6 heavy chain variable region, respectively.

Kindly replace the paragraph beginning on page 15, line 29, with the following amended paragraph:

FIG. 13. Comparisons of the amino acid sequences (SEQ ID NOS.: 55-58) of mouse and reshaped human 21.6 light chain variable regions. The amino acid residues that are part of the Chothia canonical sequences for the CDR loop structures are marked with an asterisk. RE1 shows the FRs and CDRs from the V_L region of human RE1 light chain. La and Lb are the two versions of reshaped human 21.6 V_L region. The residues in the FRs of La that differ from those in the RE1 sequence are underlined. In Lb, only the residues in the framework regions that differ from those of RE1 are shown.

Kindly replace the paragraph beginning on page 16, line 6, with the following amended paragraph:

FIG. 14. Comparisons of the amino acid sequences (SEQ ID NOS.: 59-63) of the mouse and reshaped human 21.6 heavy chain variable regions. The amino acid residues that are part of the canonical sequences for the Chothia CDR loop structures are marked with an asterisk. 2*CL shows the FRs and CDRs from the V_H region of human 21/28'CL antibody. Ha, Hb, and Hc are the three versions of reshaped human 21.6 V_H region. The residues in the FRs of Ha that differ from those in the 21/28'CL sequence are underlined. In Hb and Hc, only the residues in the framework regions that differ from those of 21/28'CL are shown.

Kindly replace the paragraph beginning on page 16, line 14, with the following amended paragraph:

FIGS. 15A and **15B.** cDNA and amino acid sequences (SEQ ID NOS.: 64-65) of the first version ("a") of reshaped human 21.6 light chain variable region.

Kindly replace the paragraph beginning on page 16, line 16, with the following amended paragraph:

FIGS. 16A and **16B.** DNA and amino acid sequences (SEQ ID NOS.: 66-67) of the first version ("a") of reshaped human 21.6 heavy chain variable region.

Kindly replace the paragraph beginning on page 16, line 18, with the following amended paragraph:

FIGS. 17A and **17B.** FIG. 17A is the 109 amino acid long sequence (SEQ ID NO.: 68) of mouse kappa V_L regions from subgroup 5 used to design the reshaped human 21.6 light chain variable regions. FIG. 17B is the 114 amino acid long

sequence (SEQ ID NO.: 69) of human V_L regions from subgroup 1 used to design the reshaped human 21.6 light chain variable regions. The sequences are further described in Table 10 *infra*.

Kindly replace the paragraph beginning on page 16, line 23, with the following amended paragraph:

FIGS. 18A and **18B**. FIG. 18A is the 125 amino acid long consensus sequence (SEQ ID NO.: 70) of mouse V_H regions from subgroup 2c used to design the reshaped human 21.6 heavy chain variable regions. FIG. 18A is the 129 amino acid long consensus sequence (SEQ ID NO.: 71) of human V_H regions from subgroup 1 used to design the reshaped human 21.6 heavy chain variable regions. The sequences are further described in Table 11 *infra*.

Kindly replace the paragraph beginning on page 228, line 24, with the following amended paragraph:

Synthesis and Humanization of Mouse Antibody HP1/2. HP1/2 is another antibody that is directed against VLA-4. The method of preparing a humanized version of this antibody for use in human subjects is described herein and is further described in U.S. Patent No. 6,602,503 assigned to Biogen, Inc., and hereby incorporated by reference in its entirety. The sequences of the humanized antibodies are provided as follows. The HP1/2 V_H DNA sequence (SEQ ID NO.: 1) and its translated amino acid sequence (SEQ ID NO.: 2) are:

Kindly replace the paragraph beginning on page 230, line 3, with the following amended paragraph:

The HP1/2 V_K DNA sequence (SEQ ID NO.: 3) and its translated amino acid sequence (SEQ ID NO.: 4) are as follows:

Kindly replace the paragraph beginning on page 231, line 26, with the following amended paragraph:

The DNA and corresponding amino acid sequence (SEQ ID NOS.: 5 and 6) of the humanized heavy chain variable region of the humanized HP1/2 antibody is:

Kindly replace the paragraph beginning on page 232, line 30, with the following amended paragraph:

The DNA and corresponding amino acid sequence (SEQ ID NOS.: 7 and 8) of the humanized light chain variable region of the humanized HP1/2 antibody

Kindly replace the paragraph beginning on page 233, line 13, with the following amended paragraph:

In addition to the above humanized HP1/2 antibody light and heavy chains, other acceptor heavy and light chains regions can also be utilized for insertion of the donor HP1/2 regions. All the following constructs contain Ser-75 (Kabat numbering). The STAW construct further contains Gln to Thr at position 77, Phe to Ala at position 78, and Ser to Trp at position 79 (Kabat numbering). The V_H DNA sequence (SEQ ID NO.: 9) and its translated amino acid sequence (SEQ ID NO.: 10) are set forth below:

Kindly replace the paragraph beginning on page 234, line 11, with the following amended paragraph:

The KAITAS construct contains the additional changes of Arg to Lys (position 66), Val to Ala (position 67), Met to Ile (position 69), Leu to Thr (position 70) and Val to Ala (position 71) (Kabat numbering. The KAITAS V_H DNA sequence (SEQ ID NO.: 11) and its translated amino acid sequence (SEQ ID NO.: 12) are set forth below:

Kindly replace the paragraph beginning on page 235, line 4, with the following amended paragraph:

The SSE construct comprises the additional changes of Ala to Ser (position 84) and Ala to Glu (position 85) (Kabat numbering). The SSE V_H DNA sequence (SEQ ID NO.: 13) and its translated amino acid sequence (SEQ ID NO.: 14) are set forth below:

Kindly replace the paragraph beginning on page 235, line 48, with the following amended paragraph:

The KRS construct comprises the additional changes of Arg to Lys (position 38) and Pro to Arg (position 40) (Kabat numbering). The KRS V_H DNA sequence (SEQ ID NO.: 15) and its translated amino acid sequence (SEQ ID NO.: 16) are set forth below:

Kindly replace the paragraph beginning on page 236, line 42, with the following amended paragraph:

The AS construct comprises the change Val to Ala at position 24 (Kabat numbering). The AS V_H DNA sequence (SEQ ID NO.: 17) and its translated amino acid sequence (SEQ ID NO.: 18) are:

Kindly replace the paragraph beginning on page 237, line 37, with the following amended paragraph:

A humanized V_K construct (VK1) comprises a Ser to Asp substitution at position 60, and a Ser for a Tyr at position 67. The DNA sequence (SEQ ID NO.: 19) and its translated amino acid sequence (SEQ ID NO.: 20) are set forth below:

Kindly replace the paragraph beginning on page 238, line 30, with the following amended paragraph:

Another V_K construct (*i.e.*, VK2) has the DQMDY sequences of the original RE1 framework restored. The DNA and corresponding amino acid sequence (SEQ ID NOS.: 21 and 22) are provided below:

Kindly replace the paragraph beginning on page 239, line 17, with the following amended paragraph:

A third V_K construct is VK3 has SVM versus DQM in the amino terminus and two other residue changes. The DNA and corresponding amino acid sequence (SEQ ID NOS.: 23 and 24) are:

Kindly replace Table 8 beginning on page 437, line 21, with the following

TABLE 8

PCR Primers for the Construction of Chimeric 21.6 Antibody
A. Light Chain Variable Region
1. Primer for reconstruction of the 5'-end (37-mer) (SEQ ID NOS.: 25 and 26)

5' C AGA <u>AAG CTT</u> GCC GCC ACC ATG AGA CCG TCT ATT CAG 3'
        *Hind*III   Kozak   M   R   P   S   I   Q
                    Consensus
                    Sequence

2. Primer for reconstruction of the 3'-end (35-mer) (SEQ ID NO.: 27)
5' CC GA<u>G GAT CC</u>A CTC ACG TTT GAT TTC CAG CTT GGT 3'   *Bam*HI   Splice donor site
B. Heavy chain variable region
1. Primer for reconstruction of the 5'-end (37-mer) (SEQ ID NOS.: 28 and 29)

5' C AGA <u>AAG CTT</u> GCC GCC ACC ATG AAA TGC AGC TGG GTC 3'
        *Hind*III   Kozak   M   K   C   S   W   V
                    Consensus
                    Sequence

2. Primer for reconstruction of the 3'-end (33-mer) (SEQ ID NO.: 30)
5' CC GA<u>G GAT CC</u>A CTC ACC TGA GGA GAC GGT GAC T 3'   *Bam*HI   Splice donor site

Kindly replace the tables beginning on page 443, line 1 and ending on page

444, with the following amended tables:

PCR primers for the construction of reshaped human 21.6 variable regions
A. Light chain variable region
1. <u>Primers for the synthesis of version "a" (SEQ ID NOS.: 31-39)</u>
21.6VLa1 (39-mer):   5' GAT GGT GAC TCT ATC TCC TAC AGA TGC AGA CAG TGA GGA 3'
21.6VLa2 (32-mer):   5' CTG TAG GAG ATA GAG TCA CCA TCA CTT GCA AG 3'
21.6VLa3 (39-mer):   5' AGG AGC TTT TCC AGG TGT CTG TTG GTA CCA AGC CAT ATA 3'
21.6VLa4 (41-mer):   5' ACC AAC AGA CAC CTG GAA AAG CTC CTA GGC TGC TCA TAC AT 3'
21.6VLa5 (40-mer):   5' GCA GGC TGC TGA TGG TGA AAG TAT AAT CTC TCC CAG ACC C 3'
21.6VLa6 (42-mer):   5' ACT TTC ACC ATC AGC AGC CTG CAG CCT GAA GAT ATT GCA ACT 3'
21.6VLa7 (59-mer):

PCR primers for the construction of reshaped human 21.6 variable regions
5' CCG AGG ATC CAC TCA CGT TTG ATT TCC ACC TTG GTG CCT TGA CCG AAC GTC CAC AGA TT 3' 2. Primers for the synthesis of version "b" 21.6VLb1 (33-mer): changes H-49 to Y-49 5' GGA AAA GCT CCT AGG CTG CTC ATA TAT TAC ACA 3' 21.6VLb2 (38-mer): changes ACC-101 to ACA-101 to destroy an *StyI* site 5' CCG AGG ATC CAC TCA CGT TTG ATT TCC ACC TTT GTG CC 3'

B. Heavy chain variable region
  1. Primers for the synthesis of version "a" (SEQ ID NOS.: 40-45)
  21.6VHa1 (51-mer):
  5' AAC CCA GTG TAT ATA GGT GTC TTT AAT GTT GAA ACC GCT AGC TTT ACA GCT 3'
 	
  21.6VHa2 (67-mer):
  5' AAA GAC ACC TAT ATA CAC TGG GTT AGA CAG GCC CCT GGC CAA AGG CTG GAG TGG ATG GGA AGG ATT G 3'
 	
  21.6VHa3 (26-mer):
  5' GAC CCG GCC CTG GAA CTT CGG GTC AT 3'
 	
  21.6VHa4 (66-mer):
  5' GAC CCG AAG TTC CAG GGC CGG GTC ACC ATC ACC GCA GAC ACC TCT GCC AGC ACC GCC TAC ATG GAA 3'
 	
  21.6VHa5 (64-mer):
  5' CCA TAG CAT AGA CCC CGT AGT TAC CAT AAT ATC CCT CTC TGG CGC AGT AGT AGA CTG CAG TGT C 3'
 	
  21.6VHa6 (63-mer):
  5' GGT AAC TAC GGG GTC TAT GCT ATG GAC TAC TGG GGT CAA GGA ACC CTT GTC ACC GTC TCC TCA 3'
 	
  2. Primer for the synthesis of version "b" (SEQ ID NO.: 46)
  21.6VHb (37-mer): changes R-44 to G-44
  5' CCA GGG CCG GGTCAC CAT CAC CAG AGA CAC CTC TGC C 3'
 	
  3. Primer for the synthesis of version "c" (SEQ ID NO.: 47)
  21.6VHc (27-mer): changes Y-98 to F-98
  5' CAG GCC CCT GGC CAA GGG CTG GAG TGG 3'

C. Both light and heavy chain variable regions
  Primers hybridizing to the flanking pUC19 vector DNA APCR1 (17-mer, sense primer) (SEQ ID NO.: 48)
  5' TAC GCA AAC CGC CTC TC 3'
 	
  APCR4 (18-mer, anti-sense primer) (SEQ ID NO.: 49)
  5' GAG TGC ACC ATA TGC GGT 3'

Kindly replace the paragraph beginning on page 445, line 3, with the following

amended paragraph:

Version "a" of a reshaped human 21.6 V$_H$ region was constructed using the same PCR methods as described for the construction of version "a" of reshaped human 21.6 V$_L$ region (Table 9). The *Hind*III-*Bam*HI DNA fragments coding for version "g" of reshaped human 425 V$_H$ region (Kettleborough *et al., supra*) and version "b" of reshaped human AUK12-20 V$_H$ region were subcloned into pUC19 vectors yielding pUC-resh425g and pUC-reshAUK12-20b, respectively. (Version "b" of AUK12-20, was derived by PCR mutagenesis of a fragment V$_H$ a425 described by Kettleborough *et al., supra*, and encodes the amino acid sequence (SEQ ID NO.: 50: QVQLVQSGAEVKKPGASVKVSCKASGYSFT SYYIH WVRQAPGQGLEWVG YIDPFNGGTSYNQKFKG KVTMTVDTSTNTAYMELSSLRSEDTAVYYCAR GGN-RFAY WGQGTLVTVSS (spaces separate FR and CDR regions)).

In compliance with 37 C.F.R. § 1.823(a), please add the attached paper copy of the "Sequence Listing" after the last page of the above-identified application.